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Relationship of plasma interleukin-6 and its genetic variants with hypertension in Hong Kong Chinese

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Introduction: Interleukin-6 (IL-6) is a pro-inflammatory cytokine, which plays a central role in insulin resistance, atherogenesis, and hepatic production of acute phase proteins, such as C-reactive protein and fibrinogen. We investigated the relationship between plasma IL-6, its genetics variants and hypertension.

Methods: Four tagging single nucleotide polymorphisms (SNPs) were genotyped in 1936 subjects from the Hong Kong Cardiovascular Risk Factor Prevalence Study–2 with a median follow-up of 6.4 years. Plasma IL-6 was measured using a high-sensitivity enzyme-linked immunosorbent assay (ELISA) in 942 subjects at follow-up.

Results: After genotyping, the SNP rs2069852 showed significant deviation from the Hardy-Weinberg equilibrium ($P<0.001$) and was excluded from all subsequent analysis. In stepwise multiple linear regression, the SNP rs1800796 was independently associated with plasma IL-6 level (beta= –0.098, P=0.002). High IL-6 levels were observed in subjects with hypertension (P=0.024), obesity (P=0.023), and the metabolic syndrome (P=0.009) after adjusting for age and sex. However, IL-6 was only independently associated with hypertension in women (P=0.002) after adjusting for other covariates. Although none of the SNPs showed significant association with prevalent hypertension, SNP rs2069837 was significantly associated with lower odds of incident hypertension (OR=0.66; 95% CI, 0.47-0.94; P=0.020). The two other SNPs, rs17147230 (OR=0.69; 95% CI, 0.48-0.99, P=0.044) and rs1800796 (OR=0.63; 95% CI, 0.39-1.00, P=0.048) also showed nominal association with lower odds of incident hypertension in women, but not men.

Conclusion: The inflammation marker, IL-6, appears to play an important role in hypertension, especially in women, in our population.

Acknowledgement: This study was funded by Hong Kong Research Grant Council grants (HKU7229/01M and HKU7626/07M), and the Sun Chieh Yeh Heart Foundation.

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Relationship of genetic variants in gene encoding adrenomedullin with hypertension and dysglycaemia in Hong Kong Chinese

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Introduction: Adrenomedullin (AM) is a vasodilatory peptide. It facilitates adipocyte differentiation and affects lipolysis and glucose uptake. Therefore, we investigated the association of common genetic variants in the adrenomedullin gene (*ADM*) with elevated blood pressure and dysglycaemia in the Hong Kong Chinese population.

Methods: Four single nucleotide polymorphisms (SNPs) in the *ADM* gene were genotyped in 1936 subjects from the Hong Kong Cardiovascular Risk Factor Prevalence Study–2, which has a median follow-up of 6.4 years. Elevated blood pressure was defined as blood pressure ≥130/85 mm Hg or taking drug treatment. Dysglycaemia included impaired fasting glucose (≥5.6 mmol/L), impaired glucose tolerance (2h glucose ≥7.8 mmol/L) or diabetes.

Results: The minor T allele of SNP rs4910118 was significantly associated with lower systolic blood pressure (β= –0.057, P=0.0079) at baseline, but not at follow-up. However, none of the SNPs was significantly associated with prevalent or incident hypertension or elevated blood pressure. Although none of the SNPs was significantly associated with prevalent dysglycaemia at baseline, the SNP rs11042725 was significantly associated with prevalent dysglycaemia at follow-up (OR=1.24; 95% CI, 1.06-1.46; P=0.0093). Among subjects without dysglycaemia at baseline, the SNP rs11042725 was a significant predictor of incident dysglycaemia in women at follow-up (hazard ratio=1.46; 95% CI, 1.15-1.86; P=0.002), but not in men, using forward stepwise Cox regression analysis.

Conclusion: Our study suggests a stronger role of genetic variants in the *ADM* gene in the development of dysglycaemia than that of hypertension in our local Chinese population. Further studies on the genetic association of AM with dysglycaemia are warranted.

Acknowledgements: This study was funded by Hong Kong Research Grant Council grants (HKU7229/01M and HKU7626/07M), and the Sun Chieh Yeh Heart Foundation.